

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Cousens, Lawrence S.
Eberhardt, Christine D.
Gray, Patrick W.
Le Trong, Hai
Tjoelker, Larry W.
Wilder, Cheryl L.
- (ii) TITLE OF INVENTION: Platelet-Activating Factor
Acetylhydrolase
- (iii) NUMBER OF SEQUENCES: 30
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
 - (B) STREET: 6300 Sears Tower, 233 South Wacker Drive
 - (C) CITY: Chicago
 - (D) STATE: Illinois
 - (E) COUNTRY: United States of America
 - (F) ZIP: 60606-6402
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER:
 - (B) FILING DATE:
 - (C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/318,905
 - (B) FILING DATE: 06-OCT-1994
- (vii) PRIOR APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 08/133,803
 - (B) FILING DATE: 06-OCT-1993
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Noland, Greta E.
 - (B) REGISTRATION NUMBER: 35,302
 - (C) REFERENCE/DOCKET NUMBER: 27866/32793
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: (312) 474-6300
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 - (C) TELEX: 25-3658

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 17 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Phe Lys Asp Leu Gly Glu Glu Asn Phe Lys Ala Leu Val Leu Ile Ala
1 5 10 15

Phe

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly Gln Thr Lys Ile Pro
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met Lys Pro Leu Val Val Phe Val Leu Gly Gly
1 5 10

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(ix) FEATURE:

- (A) NAME/KEY: Modified-site
- (B) LOCATION: group(13, 21, 27)
- (C) OTHER INFORMATION: /note= "The nucleotide at each of these positions is an inosine."

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

ACATGAATTC GGNATCYTTG NGTYTGNCRR AA

32

(2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 30 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

TATTTCTAGA AGTGTGGTGG AACTCGCTGG

30

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 32 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

CGATGAATTC AGCTTGCAGC AGCCATCAGT AC

32

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 1520 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 162..1484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

GCTGGTCGGA GGCTCGCAGT GCTGTCGGCG AGAAGCAGTC GGCTTTGGAG CGCTTGGGTC	60
GCGTTGGTGC GCGGTGGAAC GCGCCCAGGG ACCCCAGTTC CCGCGAGCAG CTCCGCGCCG	120
CGCCTGAGAG ACTAAGCTGA AACTGCTGCT CAGCTCCCAA G ATG GTG CCA CCC	173
Met Val Pro Pro	
1	
AAA TTG CAT GTG CTT TTC TGC CTC TGC GGC TGC CTG GCT GTG GTT TAT	221
Lys Leu His Val Leu Phe Cys Leu Cys Gly Cys Leu Ala Val Val Tyr	
5 10 15 20	
CCT TTT GAC TGG CAA TAC ATA AAT CCT GTT GCC CAT ATG AAA TCA TCA	269
Pro Phe Asp Trp Gln Tyr Ile Asn Pro Val Ala His Met Lys Ser Ser	
25 30 35	
GCA TGG GTC AAC AAA ATA CAA GTA CTG ATG GCT GCT GCA AGC TTT GGC	317
Ala Trp Val Asn Lys Ile Gln Val Leu Met Ala Ala Ala Ser Phe Gly	
40 45 50	
CAA ACT AAA ATC CCC CGG GGA AAT GGG CCT TAT TCC GTT GGT TGT ACA	365
Gln Thr Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr	
55 60 65	
GAC TTA ATG TTT GAT CAC ACT AAT AAG GGC ACC TTC TTG CGT TTA TAT	413
Asp Leu Met Phe Asp His Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr	
70 75 80	
TAT CCA TCC CAA GAT AAT GAT CGC CTT GAC ACC CTT TGG ATC CCA AAT	461
Tyr Pr Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn	
85 90 95 100	

AAA	GAA	TAT	TTT	TGG	GGT	CTT	AGC	AAA	TTT	CTT	GGA	ACA	CAC	TGG	CTT	509
Lys	Glu	Tyr	Phe	Trp	Gly	Leu	Ser	Lys	Phe	Leu	Gly	Thr	His	Trp	Leu	
				105					110					115		
ATG	GGC	AAC	ATT	TTG	AGG	TTA	CTC	TTT	GGT	TCA	ATG	ACA	ACT	CCT	GCA	557
Met	Gly	Asn	Ile	Leu	Arg	Leu	Leu	Phe	Gly	Ser	Met	Thr	Thr	Pro	Ala	
			120					125					130			
AAC	TGG	AAT	TCC	CCT	CTG	AGG	CCT	GGT	GAA	AAA	TAT	CCA	CTT	GTT	GTT	605
Asn	Trp	Asn	Ser	Pro	Leu	Arg	Pro	Gly	Glu	Lys	Tyr	Pro	Leu	Val	Val	
			135				140					145				
TTT	TCT	CAT	GGT	CTT	GGG	GCA	TTC	AGG	ACA	CTT	TAT	TCT	GCT	ATT	GGC	653
Phe	Ser	His	Gly	Leu	Gly	Ala	Phe	Arg	Thr	Leu	Tyr	Ser	Ala	Ile	Gly	
	150					155					160					
ATT	GAC	CTG	GCA	TCT	CAT	GGG	TTT	ATA	GTT	GCT	GCT	GTA	GAA	CAC	AGA	701
Ile	Asp	Leu	Ala	Ser	His	Gly	Phe	Ile	Val	Ala	Ala	Val	Glu	His	Arg	
	165				170				175						180	
GAT	AGA	TCT	GCA	TCT	GCA	ACT	TAC	TAT	TTC	AAG	GAC	CAA	TCT	GCT	GCA	749
Asp	Arg	Ser	Ala	Ser	Ala	Thr	Tyr	Tyr	Phe	Lys	Asp	Gln	Ser	Ala	Ala	
				185					190					195		
GAA	ATA	GGG	GAC	AAG	TCT	TGG	CTC	TAC	CTT	AGA	ACC	CTG	AAA	CAA	GAG	797
Glu	Ile	Gly	Asp	Lys	Ser	Trp	Leu	Tyr	Leu	Arg	Thr	Leu	Lys	Gln	Glu	
			200					205					210			
GAG	GAG	ACA	CAT	ATA	CGA	AAT	GAG	CAG	GTA	CGG	CAA	AGA	GCA	AAA	GAA	845
Glu	Glu	Thr	His	Ile	Arg	Asn	Glu	Gln	Val	Arg	Gln	Arg	Ala	Lys	Glu	
		215					220					225				
TGT	TCC	CAA	GCT	CTC	AGT	CTG	ATT	CTT	GAC	ATT	GAT	CAT	GGA	AAG	CCA	893
Cys	Ser	Gln	Ala	Leu	Ser	Leu	Ile	Leu	Asp	Ile	Asp	His	Gly	Lys	Pro	
		230				235					240					
GTG	AAG	AAT	GCA	TTA	GAT	TTA	AAG	TTT	GAT	ATG	GAA	CAA	CTG	AAG	GAC	941
Val	Lys	Asn	Ala	Leu	Asp	Leu	Lys	Phe	Asp	Met	Glu	Gln	Leu	Lys	Asp	
	245				250				255						260	
TCT	ATT	GAT	AGG	GAA	AAA	ATA	GCA	GTA	ATT	GGA	CAT	TCT	TTT	GGT	GGA	989
Ser	Ile	Asp	Arg	Glu	Lys	Ile	Ala	Val	Ile	Gly	His	Ser	Phe	Gly	Gly	
				265				270						275		
GCA	ACG	GTT	ATT	CAG	ACT	CTT	AGT	GAA	GAT	CAG	AGA	TTC	AGA	TGT	GGT	1037
Ala	Thr	Val	Ile	Gln	Thr	Leu	Ser	Glu	Asp	Gln	Arg	Phe	Arg	Cys	Gly	
			280					285					290			
ATT	GCC	CTG	GAT	GCA	TGG	ATG	TTT	CCA	CTG	GGT	GAT	GAA	GTA	TAT	TCC	1085
Ile	Ala	Leu	Asp	Ala	Trp	Met	Phe	Pro	Leu	Gly	Asp	Glu	Val	Tyr	Ser	
			295				300					305				
AGA	ATT	CCT	CAG	CCC	CTC	TTT	TTT	ATC	AAC	TCT	GAA	TAT	TTC	CAA	TAT	1133
Arg	Ile	Pro	Gln	Pro	Leu	Phe	Phe	Ile	Asn	Ser	Glu	Tyr	Phe	Gln	Tyr	
			310			315					320					
CCT	GCT	AAT	ATC	ATA	AAA	ATG	AAA	AAA	TGC	TAC	TCA	CCT	GAT	AAA	GAA	1181
Pro	Ala	Asn	Ile	Ile	Lys	Met	Lys	Lys	Cys	Tyr	Ser	Pro	Asp	Lys	Glu	
					330				335						340	
AGA	AAG	ATG	ATT	ACA	ATC	AGG	GGT	TCA	GTC	CAC	CAG	AAT	TTT	GCT	GAC	1229
Arg	Lys	Met	Ile	Thr	Ile	Arg	Gly	Ser	Val	His	Gln	Asn	Phe	Ala	Asp	
				345					350					355		
TTC	ACT	TTT	GCA	ACT	GGC	AAA	ATA	ATT	GGA	CAC	ATG	CTC	AAA	TTA	AAG	1277
Phe	Thr	Phe	Ala	Thr	Gly	Lys	Ile	Ile	Gly	His	Met	Leu	Lys	Leu	Lys	
			360					365					370			

GGA GAC ATA GAT TCA AAT GTA GCT ATT GAT CTT AGC AAC AAA GCT TCA	1325
Gly Asp Ile Asp Ser Asn Val Ala Ile Asp Leu Ser Asn Lys Ala Ser	
375 380 385	
TTA GCA TTC TTA CAA AAG CAT TTA GGA CTT CAT AAA GAT TTT GAT CAG	1373
Leu Ala Phe Leu Gln Lys His Leu Gly Leu His Lys Asp Phe Asp Gln	
390 395 400	
TGG GAC TGC TTG ATT GAA GGA GAT GAT GAG AAT CTT ATT CCA GGG ACC	1421
Trp Asp Cys Leu Ile Glu Gly Asp Asp Glu Met Leu Ile Pro Gly Thr	
405 410 415 420	
AAC ATT AAC ACA ACC AAT CAA CAC ATC ATG TTA CAG AAC TCT TCA GGA	1469
Asn Ile Asn Thr Thr Asn Gln His Ile Met Leu Gln Asn Ser Ser Gly	
425 430 435	
ATA GAG AAA TAC AAT TAGGATTAAA ATAGGTTTTT TAAAAA AAAA	1520
Ile Glu Lys Tyr Asn	
440	

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 441 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Val Pro Pro Lys Leu His Val Leu Phe Cys Leu Cys Gly Cys Leu	
1 5 10 15	
Ala Val Val Tyr Pro Phe Asp Trp Gln Tyr Ile Asn Pro Val Ala His	
20 25 30	
Met Lys Ser Ser Ala Trp Val Asn Lys Ile Gln Val Leu Met Ala Ala	
35 40 45	
Ala Ser Phe Gly Gln Thr Lys Ile Pro Arg Gly Asn Gly Pro Tyr Ser	
50 55 60	
Val Gly Cys Thr Asp Leu Met Phe Asp His Thr Asn Lys Gly Thr Phe	
65 70 75 80	
Leu Arg Leu Tyr Tyr Pro Ser Gln Asp Asn Asp Arg Leu Asp Thr Leu	
85 90 95	
Trp Ile Pro Asn Lys Glu Tyr Phe Trp Gly Leu Ser Lys Phe Leu Gly	
100 105 110	
Thr His Trp Leu Met Gly Asn Ile Leu Arg Leu Leu Phe Gly Ser Met	
115 120 125	
Thr Thr Pro Ala Asn Trp Asn Ser Pro Leu Arg Pro Gly Glu Lys Tyr	
130 135 140	
Pro Leu Val Val Phe Ser His Gly Leu Gly Ala Phe Arg Thr Leu Tyr	
145 150 155 160	
Ser Ala Ile Gly Ile Asp Leu Ala Ser His Gly Phe Ile Val Ala Ala	
165 170 175	
Val Glu His Arg Asp Arg Ser Ala Ser Ala Thr Tyr Tyr Phe Lys Asp	
180 185 190	

Gln Ser Ala Ala Glu Ile Gly Asp Lys Ser Trp Leu Tyr Leu Arg Thr
195 200 205

Leu Lys Gln Glu Glu Glu Thr His Ile Arg Asn Glu Gln Val Arg Gln
210 215 220

Arg Ala Lys Glu Cys Ser Gln Ala Leu Ser Leu Ile Leu Asp Ile Asp
225 230 235 240

His Gly Lys Pro Val Lys Asn Ala Leu Asp Leu Lys Phe Asp Met Glu
245 250 255

Gln Leu Lys Asp Ser Ile Asp Arg Glu Lys Ile Ala Val Ile Gly His
260 265 270

Ser Phe Gly Gly Ala Thr Val Ile Gln Thr Leu Ser Glu Asp Gln Arg
275 280 285

Phe Arg Cys Gly Ile Ala Leu Asp Ala Trp Met Phe Pro Leu Gly Asp
290 295 300

Glu Val Tyr Ser Arg Ile Pro Gln Pro Leu Phe Phe Ile Asn Ser Glu
305 310 315 320

Tyr Phe Gln Tyr Pro Ala Asn Ile Ile Lys Met Lys Lys Cys Tyr Ser
325 330 335

Pro Asp Lys Glu Arg Lys Met Ile Thr Ile Arg Gly Ser Val His Gln
340 345 350

Asn Phe Ala Asp Phe Thr Phe Ala Thr Gly Lys Ile Ile Gly His Met
355 360 365

Leu Lys Leu Lys Gly Asp Ile Asp Ser Asn Val Ala Ile Asp Leu Ser
370 375 380

Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu His Lys
385 390 395 400

Asp Phe Asp Gln Trp Asp Cys Leu Ile Glu Gly Asp Asp Glu Asn Leu
405 410 415

Ile Pro Gly Thr Asn Ile Asn Thr Thr Asn Gln His Ile Met Leu Gln
420 425 430

Asn Ser Ser Gly Ile Glu Lys Tyr Asn
435 440

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1123 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: Not Determined

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AAATATAAAT TTTAATAACA CCACACATAA ATTTCAAAC ACTTTCCTA AGTTTCTAGC

TGAAGTTT	AATGAGTGTG	TTTTTAATTT	ATTAGAAAGT	GCATTGAAGA	GAAAACATTG	120
GAAGATGAAG	GAAGGCGTTT	CAGTTAAACC	CCAAATAACT	CTGTGTTACA	CTGAGCTATG	160
AAACGGCTCC	TTCTAGCTCC	ATTTCTCCTC	AGACCTAAGT	GCTATTCCTG	ATTGTCCTTC	240
ATTGTCATTT	CCAGGGAGAA	ATGACACCAG	CACAGTGGCA	GGCCTTCCAA	TCTGGAGCAC	300
GGTCCACACA	ACTTCCGAAT	TGGTGTTCAG	TGTAAAGTGT	ATCGGAGTGC	CGAAAATGCG	360
CAGGGCATTG	CCAACTATAG	ATGCTCGGAG	TAATTCAGTG	TATTCAGAGA	ACACGGTGAA	420
ACAAGGAAAA	CCGGCCTGAC	TGGGGGGTGA	ATTGAGCAGG	GAGTAAATCT	GATCGGCATC	480
AGGTCTGCGG	AAAGGAGCTG	GTGAGCACGA	CACCACCAGG	CATTGCCTGG	CTCTCTCCGC	540
GGCGGGCTAA	GTAAACCTCG	GGTCCAGGTG	CGGGCCATGG	TCTTGGGGAG	GGTGCTGGGT	600
GCGCTCGAGC	AGGCTACGTC	GGGAGCCGCC	GCTGCTAGTG	AGAGCCGGGC	CACACACGCT	660
CCTCCCCGGT	ACCTCCTCCA	GCATCACCAG	GGGAGGAGAG	GGTCGGGCAC	AAGGCGCGCT	720
AGGCGGACCC	AGACACAGCC	GCGCGCAGCC	CACCCGCCCG	CCGCCTGCCA	GAGCTGCTCG	780
GCCCCGAGCC	AGGGGGACAG	CGGCTGGTCG	GAGGCTCGCA	GTGCTGTCCG	CGAGAAGCAG	840
TCGGGTTTGG	AGCGCTTGGG	TCGCGTTGGT	GCGCGGTGGA	ACCCCCCAGG	GACCCCAGTT	900
CCCCCGAGCA	GCTCCGCGCC	GCGCCTGAGT	GAGGAGGGGC	CCCCGGGGCG	AGGCGGGAGT	960
GGGAGGAAGG	GCACGGTCGC	CGCGCTGGAG	GTCGGGACCC	CGGAGCGGCG	ACCGGCCGGG	1020
GTGGGCTCGC	TGAGTCGCAC	CCGCTCTGCT	GGCCGGTCTT	GGGCTCACAG	TCCCTGCAGC	1080
CCTCGGAAAC	AGCGCTAGGA	TCCTTCGGGA	GAGGAGAGAT	GAC		1123

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 145..287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

GTACCAATCT	AAAACCCAGC	ACAGAAAAAT	ACATGTTTTA	TTTTTTCCAA	GTGTTACTAG	60
TACCTCAGCC	TTTCTTGATT	TGTCAGCTTA	TTTAAGGCCT	CTTCATTGCA	TACTTCTTTT	120
TTCTTTTAAT	CATCTGCTTC	GAAGGAGACT	AAGCTGAAAC	TGCTGCTCAG	CTCCCAAGAT	180
GGTGCCACCC	AAATTGCATG	TGCTTTTCTG	CCTCTGCGGC	TGCCTGGCTG	TGGTTTATCC	240
TTTGACTGG	CAATACATAA	ATCCTGTTGC	CCATATGAAA	TCATCAGGTA	AGAGGTGTAT	300
TTGTTCAAGG	TCTTGAGCAA	CTGATCTGTC	GCCATACTTC	AAGTGGGCCC	CAAGAAGTTG	360
CACATCTGCA	CATCTAAACA	AGTCTATTTT	AAAGGCTTAT	GGAGATCCTG	TATTCTC	417

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 498 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 251..372

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CATTAGGAGG TAACAGTCCA AGGCAGCTGA GAGAAAGGCT ATGTCTACTT TCATCTCTTT	60
ACCCTCCAAA ACCCTACAC AGTGTTTCAA ACAGAGAGAC CCTCAATAAT TGCATATCTT	120
ACTTGTTAGG TTGAGAAAGA AAGAAGGCCA GAACTATGG GAAGTAACTT GATTCCGTTG	180
GAATTCCTTT GCATAATAAA ATCTGATATG TAATGGATGA CAAATGAGAT AATATTTACC	240
TGTTTTTCAG CATGGGTCAA CAAAATACAA GTACTGATGG CTGCTGCAAC GTTTGGCCAA	300
ACTAAATCC CCCGGGGAAA TGGGCCTTAT TCCGTTGGTT GTACAGACTT AATGTTTGAT	360
CACACTAATA AGGTAATGCT TTGATTTATA CAACTTATCC TGATACTCTA ATATTGTCTG	420
TCGCTATGGA CCACTAGAAG GTGTTCAAAT GTGACCTTGC CCTCACCTGA GAATGACTCA	480
TTTTCGAATT TGTATTGT	498

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 433 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 130..274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

CAGCAGCCTA AAGTCTTAGA CTTTGGAAC ACAGAGGTAT TGAGTCCCAC TAATTAATAT	60
CGAAAATAGC TGCTGGAATA TGTTTGAGAC ACAACTTCTC TAAAAGTGCA TTAATTTCTT	120
TCTTAACAGG GCACCTTCTT GCGTTTATAT TATCCATCCC AAGATAATGA TCACCTTGAC	180
ACCCTTTGGA TCCCAAATAA AGAATATTTT TGGGGTCTTA GCAAATTTCT TGGAACACAC	240
TGGCTTATGG GCAACATTTT GAGGTTACTC TTTGGTAAGA TTTCTGTTGA TCCTTCTTTG	300
TAGGCTCTTG CATGTATGAA AACCTTGAAA ACAACAAGAA CTTCAAGTAG TTAAGACCAA	360
AGTA ATTTT TCTTCAGTCC AAATAGCTCC TAAAATGATA AGGAAAGTAT TTCTTTAAAG	420
CCCAGGCAAC TAC	433

(2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 486 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 164..257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

TTGGTGGGTA TCTAGTAGCA GTCTTTTAA TGAATCTACT ATTCATCCAT AAAAAAGTAG	60
ATATAAATCA GATGGGTCTG CATTTTATGC TAATGAGATA TGAATTAAAT TCACTAGCAA	120
CACTCAGAGA AAACCTTAAC TATAACCTTC CATTGTTGTC TAGGTTCAAT GACAACTCCT	180
GCAAACTGGA ATTCCCCTCT GAGGCCTGGT GAAAAATATC CACTTGTTGT TTTTCTCAT	240
GGTCTTGGGG CATTCAAGTA ATGTTTGAGA GGTGGAACAA TTTGGCTTC CAGGAATAAA	300
TGACAATTTT TTTATTCAAG AAAGAAATAG CAGAGTTTGG AATGTCATGC AGGCCCTTGT	360
CTGGAGGAGT TGGGGTTCCT CAATAATTGG CTGTGGGTCT ATTGATCAGT CCTAGACCTG	420
TCTGGTCAAG TAGTTTTTTC CTAATATCA GCTCATTGGG ATTAGCCTCA CAGCAGAGAA	480
GAAAGG	486

(2) INFORMATION FOR SEQ ID NO:14:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 363 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 113..181

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CCCCAGGCTC TACTACAGGG TGTAATGGCC TCCATGTTCC CAGTTTTATT AGTGACTCAG	60
CCTTGTAATT CATGACTGGT AGTTGTAATT CTTCCCTCTT TTTGTTTTGA AGGACACTTT	120
ATTCTGCTAT TGGCATTGAC CTGGCATCTC ATGGGTTTAT AGTTGCTGCT GTAGAACACA	180
GGTATGTTAC CTGATATAAT TGGGCTCTTT GGCCAACTAC AGGGAATGTC AATGCTCATA	240
ACTATGTTTC TAATTTTCAT AAAAGTTTAT TTAAATGTT GATGGAAGTT TCAAGTATGG	300
TAACATCATG AGCAAAAAAG GAGATTGAGT TTTATCGACT TAAAAGACTT AAAAGCACCT	360
AAC	363

(2) INFORMATION FOR SEQ ID NO:15:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 441 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 68..191

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GAAC TGAGAA ACATGGTCAG ATGAGGAAGG GAAGGAGCAT GCATAAATAA TTTTGCTTGT	60
ATTATAGAGA TAGATCTGCA TCTGCAACTT ACTATTTCAA GGACCAATCT GCTGCAGAAA	120
TAGGGGACAA GTCTTGGCTC TACCTTAGAA CCCTGAAACA AGAGGAGGAG ACACATATAC	180
GAAATGAGCA GGTACATTGC AGTGAAAGGA GAGGTGGTTG GTGACCTAAA AGCATGTACA	240
AAAGGATGAC ATTTGTTAAT TTAATTTTAC ACCTGGCAAG TTATGCTCCT AGCTCTCCTA	300
TTTCCCATTC CAAAAGATC TGTCAATAGA TTCCTGGAGC AGTAAAATTC CCTTAATGGA	360
ATATCTAGTT CATAGTAAAA ACAAAGGCAA ATACAAAAT TTGGGAGATG ACACTGAATA	420
TTCAGAATTC CTCGAGCCGG G	441

(2) INFORMATION FOR SEQ ID NO:16:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 577 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

- (ix) FEATURE:
 (A) NAME/KEY: exon
 (B) LOCATION: 245..358

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

GGTTAAGTAA ATCGTCTGAA GTCACATAGT AGGTAAGGCA AAACAGAGCC AGGATTTGGA	60
CTAAGGCTAT ACCTATGTGC AAAGCTGGGG CCTGTGTCAT TATGGTAGCA AGTAATAGTC	120
ACTAATCAGA TTTCCAGTTT ATAAGTGACC AACGATTTTT CCCAAATACA GCTTCTACCT	180
AAACTTTAAA ATAAGTGTTA TAACTTTTTA CTTTGTGATT TCCTTCTTCT AATAATTATA	240
TTAGGTACGG CAAAGAGCAA AAGAATGTTT CCAAGCTCTC AGTCTGATTG TTGACATTGA	300
TCATGGAAAG CCAGTGAAGA ATGCATTAGA TTAAAGTTT GATATGGAAC AACTGAAGGT	360
AAGCTATAAA AAGTAATTTT TCTCTTGTC TACAGTTCTT TATTGTTTTT TGTCAATTAA	420
TTTTCTGCCT ATATTGCAAG GTACAATATG ATAAAGGGCT GCAACCAGCC CCTCCCCAAT	480
CGGCACACAC AGACACACAA AGCAGTACAG GTAAAGTATT GCAGCAATGA AGAATGCATT	540

ATCTTGGACT AGATATGAAT GCAAAGTTAG TCAGTTT

577

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 396 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 108..199

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

ATCAATGTAT TTACCATCCC CATGAAATGA ACAATTATAT GATTGACAAA TCATTTCTTC	60
TAACACCACG AAATAGCTAT AAATTTATAT CATGCTTTTT CAAATAGGAC TCTATTGATA	120
GGGAAAAAAT AGCAGTAATT GGACATTCTT TTGGTGGAGC AACGGTTATT CAGACTCTTA	180
GTGAAGATCA GAGATTCAGG TAAGAAAATA AGATAGTAAA GCAAGAGAAT AGTAAATTAT	240
TGGAAGAAAT TATATTGTGA GATATAATTT TTATTCAAAT TCTTAGTGAA CGAAGGGGAT	300
CTCTTGGAGT TTATAAGGCT ATTCTTTTGC CCCCATAAAA TACTCTATAT ACATTTTCCT	360
AGGCTAAAC ATCTCCTCTC CTGCTATTAA AATCTC	396

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 519 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 181..351

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CTTACAAAGT TAATCATATC CCTTTCCCAC ATTGAAGTAT GATACCTCTT TATTCCAATC	60
AGATAACCCA TAATAAACTG GTATGGTGCG TGTCCACCAA TCCTAGCATT ATTAGGATGT	120
CCTCAATGTT GGCTAGTATG TAACCAGTTT AATTTTCATCA TTGTCAACAA ATATCTACAG	180
ATGTGGTATT GCCCTGGATG CATGGATGTT TCCACTGGGT GATGAAGTAT ATTCCAGAAT	240
TCCTCAGCCC CTCTTTTTTA TCAACTCTGA ATATTTCCAA TATCCTGCTA ATATCATAAA	300
AATGAAAAAA TGCTACTCAC CTGATAAAGA AAGAAAGATG ATTACAATCA GGTAAGTATT	360
AGTGACTTAT TTCATTATGT GAAACAAACT TGAAGCTTGG GTAAATATCA ATCGATATCA	420
TTTGGTAACT ATTAAAGAAT TGCTGAATTG GTTGTTTAGA CTTTCAATAA GGAGAGAATT	480
AGATAATCTC AGTTTCTAAG TACATTTAGT CTACTCTTT	519

(2) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 156..304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

TGAAACACAT CTAAGTAGAT CAAATTACAA GTTTTATTTT TTCTTTGGTT TTCAGTAAAC	60
AGACCAACAA GACCACTACC TTTCCTTACA CTCTAACTAA AAAAATAATA ATTTTATCAA	120
ACAATGTGAC TTTTAAATGT CTTGTTCTCT TTTAGGGGTT CAGTCCACCA GAATTTTGCT	180
GACTTCACTT TTGCAACTGG CAAAATAATT GGACACATGC TCAAATTAAA GGGAGACATA	240
GATTCAAATG TAGCTATTGA TCTTAGCAAC AAAGCTTCAT TAGCATTCTT ACAAAGCAT	300
TTAGGTAAGA AACTATTTTT TTCATGACCT AAACCGAGAT GAATCTCGAG GACAAAGCTG	360
TCTATCTTAA TACAGCTTTA GTACTATTTA AACTATTTCC AGTTGGTTTA CAATGGAACA	420
AAGCACTATA TCAATTTGAA AACAGAAATT TGAGAAAGTC AATTTTGCTG CTTTACATCT	480
CTATATCATA GAAAGCAAAT CAACTGTAA AGGTAATATT CTTTGTATGA GCTAGACTGA	540
CTCATGTGAG GATATCGAAC GACGGTGCT	569

(2) INFORMATION FOR SEQ ID NO:20:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 469 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(ix) FEATURE:

- (A) NAME/KEY: exon
- (B) LOCATION: 137..253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

GATACAGAGG CACATCGTCT CTACCATCCT AACGGAAGTT GTGTAATTTG TAAATCTTTA	60
TTGCCACCTA GGGGCATCCA AACTGTTTAA TGCTCTCAAA AGTTTAATAT GTTGATTAAC	120
ACTTTATATT TTATAGGACT TCATAAGAT TTTGATCAGT GGGACTGCTT GATTGAAGGA	180
GATGATGAGA ATCTTATTCC AGGGACCAAC ATTAACACAA CCAATCAACA CATCATGTTA	240
CAGAACTCTT CAGGAATAGA GAAATACAAT TAGGATTAAA ATAGGTTTTT TAAAGTCTT	300
GTTTCAAAAC TGTCTAAAAT TATGTGTGTG TGTGTGTGTG TGTGTGTGTG AGAGAGAGA	360
AGAGAGAGAG AGAGAGAATT TTAATGTATT TTCCCAAAGG ACTCATATT TAAATGTAG	420

GCTATACTGT AATCGTGATT GAAGCTTGGA CTAAGAATTT TTTCCCTTT

469

(2) INFORMATION FOR SEQ ID NO:21:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1494 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 117..1436

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

GGCAGGAGCT AGGATCTGAC TCGCTCTGGT GGCATTGCTG CGCTCAGGGT TCTGGGTATC	60
CGGGAGTCAG TGCAGTGACC AGAACATCAA ACTGAAGCCA CTGCTCAGCT CCTAAG	116
ATG GTA CCA CTC AAA CTG CAG GCG CTT TTC TGC CTC CTC TGC TGC CTC Met Val Pro Leu Lys Leu Gln Ala Leu Phe Cys Leu Leu Cys Cys Leu	164
CCA TGG GTC CAT CCT TTT CAC TGG CAA GAC ACA TCT TCT TTT GAC TTC Pro Trp Val His Pro Phe His Trp Gln Asp Thr Ser Ser Phe Asp Phe	212
AGG CCG TCA GTA ATG TTT CAC AAG CTC CAA TCG GTG ATG TCT GCT GCC Arg Pro Ser Val Met Phe His Lys Leu Gln Ser Val Met Ser Ala Ala	260
GGC TCT GGC CAT AGT AAA ATC CCC AAA GGA AAT GGA TCG TAC CCC GTC Gly Ser Gly His Ser Lys Ile Pro Lys Gly Asn Gly Ser Tyr Pro Val	308
GGT TGT ACA GAT CTG ATG TTC GGT TAT GGG AAT GAG AGC GTC TTC GTG Gly Cys Thr Asp Leu Met Phe Gly Tyr Gly Asn Glu Ser Val Phe Val	356
CGT TTG TAC TAC CCA GCT CAA GAT CAA GGT CGC CTC GAC ACT GTT TGG Arg Leu Tyr Tyr Pro Ala Gln Asp Gln Gly Arg Leu Asp Thr Val Trp	404
ATC CCA AAC AAA GAA TAT TTT TTG GGT CTT AGT ATA TTT CTT GGA ACA Ile Pro Asn Lys Glu Tyr Phe Leu Gly Leu Ser Ile Phe Leu Gly Thr	452
CCC AGT ATT GTA GGC AAT ATT TTA CAC CTC TTA TAT GGT TCT CTG ACA Pro Ser Ile Val Gly Asn Ile Leu His Leu Leu Tyr Gly Ser Leu Thr	500
ACT CCT GCA AGC TGG AAT TCT CCT TTA AGG ACT GGA GAA AAA TAC CCG Thr Pro Ala Ser Trp Asn Ser Pro Leu Arg Thr Gly Glu Lys Tyr Pro	548
CTC ATT GTC TTT TCT CAT GGT CTC GGA GCC TTC AGG ACG ATT TAT TCT Leu Ile Val Phe Ser His Gly Leu Gly Ala Phe Arg Thr Ile Tyr Ser	596
GCT ATT GGC ATT GGC TTG GCA TCT AAT GGG TTT ATA GTG GCC ACT GTC Ala Ile Gly Ile Gly Leu Ala Ser Asn Gly Phe Ile Val Ala Thr Val	644

[illegible]

TTTAAAAGTA GAGTGACATG ACAGAGAG

1494

(2) INFORMATION FOR SEQ ID NO:22:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2191 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 92..1423

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

CCGCGCGCTC CGGCCGGGGG ACCCTGGTTC CGGCGAGCGG CTCAGCGCGG CGCCCGGAAG	60
TTTAAGCTGA AACCCTGCT CAGCTTCCAA G ATG TTG CCA CCC AAA CTG CAT	112
Met Leu Pro Pro Lys Leu His	
1 5	
GCG CTT TTC TGC CTC TGC AGC TGC CTC ACA CTG GTT CAT CCT ATT GAC	160
Ala Leu Phe Cys Leu Cys Ser Cys Leu Thr Leu Val His Pro Ile Asp	
10 15 20	
TGG CAA GAC CTA AAT CCT GTT GCC CAT ATT AGA TCA TCA GCA TGG GCC	208
Trp Gln Asp Leu Asn Pro Val Ala His Ile Arg Ser Ser Ala Trp Ala	
25 30 35	
AAT AAA ATA CAA GCT CTG ATG GCT GCT GCA AGT ATT AGG CAA AGT AGA	256
Asn Lys Ile Gln Ala Leu Met Ala Ala Ala Ser Ile Arg Gln Ser Arg	
40 45 50 55	
ATT CCC AAA GGA AAT GGA TCT TAT TCT GTC GGT TGT ACA GAT TTG ATG	304
Ile Pro Lys Gly Asn Gly Ser Tyr Ser Val Gly Cys Thr Asp Leu Met	
60 65 70	
TTT GAT TAT ACT AAT AAG GGC ACC TTT TTG CGT TTG TAT TAT CCA TCG	352
Phe Asp Tyr Thr Asn Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro Ser	
75 80 85	
CAA GAG GAT GAC CAC TCT GAC ACG CTT TGG ATC CCA AAC AAA GAA TAT	400
Gln Glu Asp Asp His Ser Asp Thr Leu Trp Ile Pro Asn Lys Glu Tyr	
90 95 100	
TTT TTT GGT CTT AGT AAA TAT CTT GGA ACA CCC TGG CTT ATG GGC AAA	448
Phe Phe Gly Leu Ser Lys Tyr Leu Gly Thr Pro Trp Leu Met Gly Lys	
105 110 115	
ATA TTG AGC TTC TTT TTT GGT TCA GTG ACA ACT CCT GCG AAC TGG AAT	496
Ile Leu Ser Phe Phe Phe Gly Ser Val Thr Thr Pro Ala Asn Trp Asn	
120 125 130 135	
TCC CCT CTG AGG ACT GGT GAA AAA TAT CCA CTG ATT GTT TTT TCT CAT	544
Ser Pro Leu Arg Thr Gly Glu Lys Tyr Pro Leu Ile Val Phe Ser His	
140 145 150	
GGT CTT GGA GCA TTC CGG ACA ATT TAT TCT GCT ATT GGC ATT GAT CTA	592
Gly Leu Gly Ala Phe Arg Thr Ile Tyr Ser Ala Ile Gly Ile Asp Leu	
155 160 165	

GCA	TCA	CAT	GGG	TTC	ATC	GTT	GCT	GCT	ATA	GAA	CAC	AGA	GAT	GGA	TCC	640
Ala	Ser	His	Gly	Phe	Ile	Val	Ala	Ala	Ile	Glu	His	Arg	Asp	Gly	Ser	
		170					175					180				
GCC	TCT	GCG	ACT	TAC	TAT	TTC	AAG	GAC	CAG	TCT	GCT	GCA	GAA	ATA	GGG	688
Ala	Ser	Ala	Thr	Tyr	Tyr	Phe	Lys	Asp	Gln	Ser	Ala	Ala	Glu	Ile	Gly	
		185				190					195					
AAC	AAA	TCT	TGG	TCT	TAT	CTT	CAA	GAA	CTA	AAA	CCA	GGG	GAT	GAG	GAG	736
Asn	Lys	Ser	Trp	Ser	Tyr	Leu	Gln	Glu	Leu	Lys	Pro	Gly	Asp	Glu	Glu	
200					205					210					215	
ATA	CAT	GTT	CGA	AAT	GAG	CAG	GTA	CAG	AAA	AGG	GCA	AAG	GAG	TGC	TCC	784
Ile	His	Val	Arg	Asn	Glu	Gln	Val	Gln	Lys	Arg	Ala	Lys	Glu	Cys	Ser	
				220					225					230		
CAA	GCT	CTC	AAC	TTG	ATT	CTG	GAC	ATT	GAT	CAT	GGA	AGG	CCA	ATT	AAG	832
Gln	Ala	Leu	Asn	Leu	Ile	Leu	Asp	Ile	Asp	His	Gly	Arg	Pro	Ile	Lys	
			235					240					245			
AAT	GTA	CTA	GAC	TTA	GAG	TTT	GAT	GTG	GAA	CAA	CTG	AAG	GAC	TCT	ATT	880
Asn	Val	Leu	Asp	Leu	Glu	Phe	Asp	Val	Glu	Gln	Leu	Lys	Asp	Ser	Ile	
		250					255					260				
GAC	AGG	GAT	AAA	ATA	GCA	GTA	ATT	GGA	CAT	TCT	TTT	GGT	GGA	GCC	ACA	928
Asp	Arg	Asp	Lys	Ile	Ala	Val	Ile	Gly	His	Ser	Phe	Gly	Gly	Ala	Thr	
		265				270					275					
GTT	CTT	CAG	GCT	CTT	AGT	GAA	GAC	CAG	AGA	TTT	AGG	TGC	GGG	ATT	GCC	976
Val	Leu	Gln	Ala	Leu	Ser	Glu	Asp	Gln	Arg	Phe	Arg	Cys	Gly	Ile	Ala	
280					285					290					295	
TTG	GAT	GCA	TGG	ATG	CTT	CCA	CTG	GAT	GAT	GCA	ATA	TAT	TCC	AGA	ATC	1024
Leu	Asp	Ala	Trp	Met	Leu	Pro	Leu	Asp	Asp	Ala	Ile	Tyr	Ser	Arg	Ile	
				300					305					310		
CCT	CAG	CCC	CTC	TTT	TTT	ATT	AAC	TCG	GAA	CGG	TTC	CAA	TTT	CCT	GAG	1072
Pro	Gln	Pro	Leu	Phe	Phe	Ile	Asn	Ser	Glu	Arg	Phe	Gln	Phe	Pro	Glu	
			315					320					325			
AAT	ATC	AAA	AAA	ATG	AAA	AAA	TGC	TAC	TCA	CCT	GAC	AAA	GAA	AGA	AAA	1120
Asn	Ile	Lys	Lys	Met	Lys	Lys	Cys	Tyr	Ser	Pro	Asp	Lys	Glu	Arg	Lys	
		330					335					340				
ATG	ATT	ACA	ATC	AGG	GGT	TCA	GTC	CAT	CAG	AAC	TTT	GCT	GAT	TTC	ACT	1168
Met	Ile	Thr	Ile	Arg	Gly	Ser	Val	His	Gln	Asn	Phe	Ala	Asp	Phe	Thr	
		345				350					355					
TTT	ACA	ACT	GGC	AAA	ATA	GTT	GGA	TAC	ATA	TTC	ACA	TTA	AAA	GGA	GAT	1216
Phe	Thr	Thr	Gly	Lys	Ile	Val	Gly	Tyr	Ile	Phe	Thr	Leu	Lys	Gly	Asp	
360					365					370					375	
ATA	GAT	TCA	AAT	GTA	GCA	ATT	GAT	CTT	TGC	AAC	AAA	GCT	TCA	TTG	GCA	1264
Ile	Asp	Ser	Asn	Val	Ala	Ile	Asp	Leu	Cys	Asn	Lys	Ala	Ser	Leu	Ala	
				380					385					390		
TTT	TTA	CAA	AAG	CAT	TTA	GGA	CTG	CGG	AAA	GAT	TTT	GAT	CAG	TGG	GAT	1312
Phe	Leu	Gln	Lys	His	Leu	Gly	Leu	Arg	Lys	Asp	Phe	Asp	Gln	Trp	Asp	
			395					400					405			
TCT	TTG	ATT	GAA	GGA	AAA	GAC	GAA	AAT	CTT	ATG	CCA	GGG	ACC	AAC	ATT	1360
Ser	Leu	Ile	Glu	Gly	Lys	Asp	Glu	Asn	Leu	Met	Pro	Gly	Thr	Asn	Ile	
		410					415					420				
AAC	ATC	ACC	AAC	GAA	CAT	GAC	ACT	CTA	CAG	AAC	TCT	CCA	GAA	GCA	GAG	1408
Asn	Ile	Thr	Asn	Glu	His	Asp	Thr	Leu	Gln	Asn	Ser	Pro	Glu	Ala	Glu	
		425				430					435					

AAA TCG AAT TTA GAT TAAAGCACT TTTTAAAGA TCTTGTTTAA AAAGTGTCAA 1463
 Lys Ser Asn Leu Asp
 440

AAAATGTGTG TATGACTTTT AATATATTTT CTCAAATAAC TCATATTGGA AAATGTAGGC 1523
 TATCCCATAA AAGTGATTGA AGCTTGGACT AGGAGGTTTT TTTCTTTAAA GAAAGATTGG 1583
 TGTCTATCGA AATCATGCCA GCCTAAATTT TAATTTTACT AAAATGATGC TGTGTCAAAA 1643
 TTAATAACTA CTTTTACATT CTTTAATGGA CAAGTATAAC AGGCACAAGG CTAATGAAAA 1703
 CGTGTTGCAA TGACATAACA ATCCCTAAAA ATACAGATGT TCTTGCCTCT TTTTCTATT 1763
 ATAATTGAGT TTTAGCAACA TGTTATGCTA GGTAGAATTT GGAAGCACTT CCCTTTGACT 1823
 TTTGGTCATG ATAAGAAAAA TTAGATCAAG CAAATGATAA AAGCAGTGTT TTACCAAGGA 1883
 TTAGGGATAC TGAACAATTT CACTATGGTA ACTGAATGGG GAGTGACCAA GGGTAAAAAT 1943
 ATTAAAGCCA AGGCAAAGGC AGCAGATTAG AATGGATTAA AGAGAGTTTA TAATTTGTTT 2003
 GCATTTACTT GATGGTTTAT CTCATGGATT CATGAGTCAA GAAAGGTGCG TAGGACAGGC 2063
 CAGGGATTCC AGTTATAACA CATTATTCAC CCAAAGGGTT CTTTAATTCT GTATGAGTAT 2123
 TGGGAGTGGA TTAGCACAAT AGAGGCATAT GTTGCTTTAA AAAAAAAAAA AAAAAAAAAA 2183
 AAAAAAAAAA 2191

(2) INFORMATION FOR SEQ ID NO:23:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1533 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 62..1394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

CCGCGAGCAG TTCACCGCGG CGTCCGGAAG GTTAAGCTGA AACGGCAGCT CAGCTTCGGA 60
 G ATG TTA CCG TCC AAA TTG CAT GCG CTT TTC TGC CTC TGC ACC TGC 106
 Met Leu Pro Ser Lys Leu His Ala Leu Phe Cys Leu Cys Thr Cys
 1 5 10 15

CTT GCA CTG GTT TAT CCT TTT GAC TGG CAA GAC CTG AAT CCA GTT GCC 154
 Leu Ala Leu Val Tyr Pro Phe Asp Trp Gln Asp Leu Asn Pro Val Ala
 20 25 30

TAT ATT GAA TCA CCA GCA TGG GTC AGT AAG ATA CAA GCT CTG ATG GCT 202
 Tyr Ile Glu Ser Pro Ala Trp Val Ser Lys Ile Gln Ala Leu Met Ala
 35 40 45

GCT GCA AAC ATT GGT CAA TCT AAA ATC CCC AGA GGA AAT GGA TCT TAT 250
 Ala Ala Asn Ile Gly Gln Ser Lys Ile Pro Arg Gly Asn Gly Ser Tyr
 50 55 60

TCC Ser	GTC Val	GGT Gly	TGT Cys	ACA Thr	GAC Asp	TTG Leu	ATG Met	TTT Phe	GAT Asp	TAC Tyr	ACT Thr	AAT Asn	AAG Lys	GGC Gly	ACC Thr	298
65						70					75					
TTC Phe	TTG Leu	CGT Arg	TTG Leu	TAT Tyr	TAT Tyr	CCA Pro	TCT Ser	CAA Gln	GAT Asp	GAT Asp	GAT Asp	CAC His	TCC Ser	GAC Asp	ACC Thr	346
80					85					90					95	
CTT Leu	TGG Trp	ATC Ile	CCA Pro	AAC Asn	AAA Lys	GAA Glu	TAT Tyr	TTT Phe	TTG Leu	GGT Gly	CTT Leu	AGT Ser	AAA Lys	TTT Phe	CTT Leu	394
				100					105					110		
GGA Gly	ACA Thr	CAC His	TGG Trp	CTT Leu	GTG Val	GGC Gly	AAA Lys	ATT Ile	ATG Met	GGC Gly	TTA Leu	TTC Phe	TTC Phe	GGT Gly	TCA Ser	442
			115					120					125			
ATG Met	ACA Thr	ACT Thr	CCT Pro	GCA Ala	GCC Ala	TGG Trp	AAT Asn	GCA Ala	CAT His	CTG Leu	AGG Arg	ACT Thr	GGG Gly	GAA Glu	AAA Lys	490
		130					135					140				
TAC Tyr	CCA Pro	CTA Leu	ATT Ile	ATT Ile	TTT Phe	TCT Ser	CAT His	GGT Gly	CTT Leu	GGA Gly	GCA Ala	TTC Phe	AGG Arg	ACG Thr	ATT Ile	538
	145					150					155					
TAT Tyr	TCT Ser	GCT Ala	ATT Ile	GGC Gly	ATT Ile	GAT Asp	CTG Leu	GCA Ala	TCC Ser	CAC His	GGG Gly	TTT Phe	ATA Ile	GTT Val	GCT Ala	586
160					165					170					175	
GCT Ala	GTA Val	GAA Glu	CAC His	AGG Arg	GAT Asp	GGC Gly	TCT Ser	GCA Ala	TCC Ser	TCG Ser	ACA Thr	TAC Tyr	TAT Tyr	TTC Phe	AAG Lys	634
				180					185					190		
GAC Asp	CAG Gln	TCT Ser	GCT Ala	GTA Val	GAA Glu	ATA Ile	GGC Gly	AAC Asn	AAG Lys	TCT Ser	TGG Trp	CTC Leu	TAT Tyr	CTC Leu	AGA Arg	682
			195					200					205			
ACC Thr	CTG Leu	AAG Lys	CGA Arg	GGA Gly	GAG Glu	GAG Glu	GAG Glu	TTT Phe	CCT Pro	TTA Leu	CGA Arg	AAT Asn	GAG Glu	CAG Gln	TTA Leu	730
		210					215					220				
CGG Arg	CAA Gln	CGA Arg	GCA Ala	AAG Lys	GAA Glu	TGT Cys	TCT Ser	CAA Gln	GCT Ala	CTC Leu	AGT Ser	TTG Leu	ATT Ile	CTG Leu	GAC Asp	778
		225				230					235					
ATT Ile	GAT Asp	CAC His	GGG Gly	AGG Arg	CCA Pro	GTG Val	ACG Thr	AAT Asn	GTA Val	CTA Leu	GAT Asp	TTA Leu	GAG Glu	TTT Phe	GAT Asp	826
240					245				250						255	
GTG Val	GAA Glu	CAG Gln	CTG Leu	AAG Lys	GAC Asp	TCT Ser	ATT Ile	GAT Asp	AGG Arg	GAT Asp	AAA Lys	ATA Ile	GCC Ala	ATT Ile	ATT Ile	874
				260					265					270		
GGA Gly	CAT His	TCT Ser	TTT Phe	GGT Gly	GGA Gly	GCC Ala	ACA Thr	GTT Val	ATT Ile	CAG Gln	ACT Thr	CTT Leu	AGT Ser	GAA Glu	GAC Asp	922
			275					280					285			
CAG Gln	AGA Arg	TTC Phe	AGG Arg	TGT Cys	GGC Gly	ATT Ile	GCT Ala	CTG Leu	GAT Asp	GCA Ala	TGG Trp	ATG Met	TTT Phe	CCC Pro	GTG Val	970
		290					295					300				
GGT Gly	GAT Asp	GAA Glu	GTA Val	TAT Tyr	TCC Ser	AGA Ile	ATT Pro	CCT Gln	CAA Pro	CCC Pro	CTC Phe	TTT Phe	TTT Phe	ATC Ile	AAC Asn	1018
	305					310					315					
TCG Ser	GAA Glu	CGA Arg	TTC Phe	CAA Gln	TAC Tyr	CCT Pr	TCT Ser	AAT Asn	ATC Ile	ATA Arg	ATG Met	AAA Lys	AAA Lys	TGC Cys		1066
320					325					330				335		

TTC TTA CCT GAT AGA GAA CGA AAA ATG ATT ACA ATC AGG GGT TCG GTC	1114
Phe Leu Pro Asp Arg Glu Arg Lys Met Ile Thr Ile Arg Gly Ser Val	
340 345 350	
CAT CAG AAT TTT GTT GAC TTC ACT TTT GCC ACT AGC AAA ATA ATT GGC	1162
His Gln Asn Phe Val Asp Phe Thr Phe Ala Thr Ser Lys Ile Ile Gly	
355 360 365	
TAC CTA TTC ACA CTG AAA GGA GAC ATC GAT TCC AAT GTA GCC ATC AGC	1210
Tyr Leu Phe Thr Leu Lys Gly Asp Ile Asp Ser Asn Val Ala Ile Ser	
370 375 380	
CTT AGC AAC AAA GCT TCC TTA GCG TTC TTA CAA AAA CAT TTA GGA CTT	1258
Leu Ser Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly Leu	
385 390 395	
CAG AAA GAT TTT GAT CAG TGG GAT TCT TTA GTT GAA GGC GAA GAT CAC	1306
Gln Lys Asp Phe Asp Gln Trp Asp Ser Leu Val Glu Gly Glu Asp His	
400 405 410 415	
AAT CTT ATT CCA GGG ACC AAC ATT AAC ACA ACC AAC CAC CAA GCC ATT	1354
Asn Leu Ile Pro Gly Thr Asn Ile Asn Thr Thr Asn His Gln Ala Ile	
420 425 430	
CTG CAG AAC TCC ACA GGA ATA GAG AGA CCA AAT TTA GAT T AAAAGAGCTT	1404
Leu Gln Asn Ser Thr Gly Ile Glu Arg Pro Asn Leu Asp	
435 440	
TTTAAAAAGT TTTGTTTACG AACTTGTCTA AAAGTGTGTG TGTGTATGAT TTAAATGTAT	1464
TTTCTCAAAT AGCTCATATT AAAAAATGTA GGCTATAGCA CAAAAAATAA AAAAAAATAA	1524
AAAAAATAA	1533

(2) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1876 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 468..1734

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

CGGCGGGCTG CTGGCCCTTC CCGGCTGTTC GTAGAGCCGG ATCCTGCAGC GCCCCTGAGA	60
CGAACCGCCC CGATGCGGTG CTCCTCAGCG CCACGGGACG CAGCCGGGGC CGGCCGTGTT	120
GGCGCAGCTC CCACGACGTA CGCTTCCTTT CCAGGCTCGA GGAAAGCCTC TCCCACAAAC	180
ACCGTCCCAG CTGGGAAGTG AGGCGGAGTT TTGGTCCCTC CCCTCCGGCA GCGCCCGGCA	240
TTCCGTCCGT CCGTCCGTCC GTCCGTGCGG CGCACGGCGC CCTGCAGAGC CGGGACACCG	300
CAGCAGGGTA GGAGGACCCG GAGGTGGTGT GCAGCCACAG GTTTCATCC TGCCCCCACC	360
TCCCGGGGAG CAGCCCTGTG CTATACCCAA CCCCCGCAC AGAGCACTGA CCGGCTGCT	420

GCCTGCCTGC	ACCCCGCCGT	GGGACCTTCT	GCTCTTCCCA	ACAACTG	ATG	GCA	TCG	476
					Met	Ala	Ser	
					1			
CTG	TGG	GTG	AGA	GCC	AGG	AGG	GTG	524
Leu	Trp	Val	Arg	Ala	Arg	Arg	Val	
	5					10		
TTC	TCG	GCG	AAG	GCG	GCG	ACG	GAG	572
Phe	Ser	Ala	Lys	Ala	Ala	Thr	Glu	
20				25			35	
GGC	TAT	CGG	ATC	CCC	GCC	GGG	AAG	620
Gly	Tyr	Arg	Ile	Pro	Ala	Gly	Lys	
				40			50	
GAT	CTG	ATG	ACC	GGC	GAC	GCG	GCC	668
Asp	Leu	Met	Thr	Gly	Asp	Ala	Ala	
			55				60	
TAC	CTA	TCG	TGT	GAC	GAC	ACA	GAT	716
Tyr	Leu	Ser	Cys	Asp	Asp	Thr	Asp	
		70					75	
GAT	AAA	GAG	TAC	TAC	CAG	GGG	CTG	764
Asp	Lys	Glu	Tyr	Tyr	Gln	Gly	Leu	
	85					90		
GCC	CTG	GGA	GAA	AGG	CTT	TTC	CAG	812
Ala	Leu	Gly	Glu	Arg	Leu	Phe	Gln	
100					105			
CCT	GCA	AAA	TCA	AAC	GCT	GCT	TTT	860
Pro	Ala	Lys	Ser	Asn	Ala	Ala	Phe	
				120				
CTC	GTT	TTT	TCC	CAT	GGA	CTT	GGA	908
Leu	Val	Phe	Ser	His	Gly	Leu	Gly	
			135				140	
ATC	TGC	ATA	GAG	ATG	GCT	TCT	CAA	956
Ile	Cys	Ile	Glu	Met	Ala	Ser	Gln	
	150						155	
CAC	AGA	GAT	GAA	TCG	GCT	TCA	GCA	1004
His	Arg	Asp	Glu	Ser	Ala	Ser	Ala	
	165					170		
GAT	TCT	GAG	CCA	GAG	GAG	GAT	CAA	1052
Asp	Ser	Glu	Pro	Glu	Glu	Asp	Gln	
180				185				
ATC	TAC	TAC	AGG	AAG	CTC	AGA	GCA	1100
Ile	Tyr	Tyr	Arg	Lys	Leu	Arg	Ala	
				200				
CAC	AAG	CAG	GTA	CAG	CAG	AGA	GCA	1148
His	Lys	Gln	Val	Gln	Gln	Arg	Ala	
			215					
CTC	ATT	CTT	AAG	ATC	AGT	TCA	GGA	1196
Leu	Ile	Leu	Lys	Ile	Ser	Ser	Gly	
		230					235	
TCA	GAC	TTT	GAC	TGG	AAC	CAC	CTG	1244
Ser	Asp	Phe	Asp	Trp	Asn	His	Leu	
	245					250		

ATA GCT GTG ATG GGA CAC TCT TTT GGT GGT GCT ACA GTT ATT GAG AGC Ile Ala Val Met Gly His Ser Phe Gly Gly Ala Thr Val Ile Glu Ser 260 265 270 275	1292
CTC AGC AAA GAA ATT AGA TTT AGG TGT GGC ATT GCC CTT GAT GCG TGG Leu Ser Lys Glu Ile Arg Phe Arg Cys Gly Ile Ala Leu Asp Ala Trp 280 285 290	1340
ATG CTC CCG GTA GGC GAT GAC ACT TAC CAA AGC AGT GTG CAG CAA CCA Met Leu Pro Val Gly Asp Asp Thr Tyr Gln Ser Ser Val Gln Gln Pro 295 300 305	1388
CTG CTC TTT ATT AAT TCC GAA AAA TTC CAG TGG GCT GCC AAT ATC TTA Leu Leu Phe Ile Asn Ser Glu Lys Phe Gln Trp Ala Asn Ile Leu 310 315 320	1436
AAG ATG AAG AAG CTT AGC TCC AAT GAT ACC AAC AAG AAA ATG ATC ACC Lys Met Lys Lys Leu Ser Ser Asn Asp Thr Asn Lys Lys Met Ile Thr 325 330 335	1484
ATC AAA GGA TCG GTA CAT CAG AGC TTT CCT GAT TTT ACT TTT GTG AGT Ile Lys Gly Ser Val His Gln Ser Phe Pro Asp Phe Thr Phe Val Ser 340 345 350 355	1532
GGA GAA ATC ATT GGA AAG TTT TTC AAG TTA AAA GGA GAA ATA GAC CCA Gly Glu Ile Ile Gly Lys Phe Phe Lys Leu Lys Gly Glu Ile Asp Pro 360 365 370	1580
AAT GAA GCT ATT GAT ATA TGC AAC CAC GCT TCA TTG GCC TTC CTG CAG Asn Glu Ala Ile Asp Ile Cys Asn His Ala Ser Leu Ala Phe Leu Gln 375 380 385	1628
AAA CAT CTG AGT CTT AAG AGA GAT TTT GAT AAG TGG GAT TCA CTC GIG Lys His Leu Ser Leu Lys Arg Asp Phe Asp Lys Trp Asp Ser Leu Val 390 395 400	1676
GAT GGC ATA GGA CCC AAT GTT ATT TCT GGT ACC AAT ATC GAC TTA TCT Asp Gly Ile Gly Pro Asn Val Ile Ser Gly Thr Asn Ile Asp Leu Ser 405 410 415	1724
CCA ACT GAG T AAGGAGTACA AGAAGTACTG CAAAGGCCAC CAGCAGCAGG Pro Thr Glu 420	1774
ACACCAACGT TGGCCACACA TTGCTTGGAG CTGAGATAGC ACTGGCCTCC CACACAGCTT	1834
TTGGAGTGTG AAACAACAAA AAAAAAATC ACAGGGGAGC CG	1876

(2) INFORMATION FOR SEQ ID NO:25:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 517 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 2..514

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

G GGG CAT TCT TTT GGA GGA GCA ACA GTT TTT CAA GCC CTA AGT GAA	46
Gly His Ser Phe Gly Gly Ala Thr Val Phe Gln Ala Leu Ser Glu	
1 5 10 15	
GAC CAG AGA TTC AGA TGT GGG ATT GCC CTT GAT CCG TCG ATG TTT CCC	94
Asp Gln Arg Phe Arg Cys Gly Ile Ala Leu Asp Pro Trp Met Phe Pro	
20 25 30	
GTG AGT GAG GAG CTG TAC TCC AGA GTT CCT CAG CCT CTC TTC TTT ATC	142
Val Ser Glu Glu Leu Tyr Ser Arg Val Pro Gln Pro Leu Phe Phe Ile	
35 40 45	
AAC TCT GCC GAA TTC CAG ACT CCA AAG GAC ATT GCA AAA ATG AAA AAC	190
Asn Ser Ala Glu Phe Gln Thr Pro Lys Asp Ile Ala Lys Met Lys Asn	
50 55 60	
TTC TAC CAG CCT GAC AAG GAA AGG AAA ATG ATT ACG ATC AAG GGC TCA	238
Phe Tyr Gln Pro Asp Lys Glu Arg Lys Met Ile Thr Ile Lys Gly Ser	
65 70 75	
GTG CAC CAG AAT TTT GCT GAC GGG ACT TTT GTA ACT GGC AAA ATA ATT	286
Val His Gln Asn Phe Ala Asp Gly Thr Phe Val Thr Gly Lys Ile Ile	
80 85 90 95	
GGA AAC AAG CTG TCA CTG AAA GGA GAC ATA GAC TCC AGA GTT GCC ATA	334
Gly Asn Lys Leu Ser Leu Lys Gly Asp Ile Asp Ser Arg Val Ala Ile	
100 105 110	
GAC CTC ACC AAC AAG GCT TCC TTG GCT TTC TTA CAA AAA CAT TTA GGA	382
Asp Leu Thr Asn Lys Ala Ser Leu Ala Phe Leu Gln Lys His Leu Gly	
115 120 125	
CTT CAT AAA GAC TTT GAT CAG TGG GAC TGT CTG GTG GAG GGA GAG AAC	430
Leu His Lys Asp Phe Asp Gln Trp Asp Cys Leu Val Glu Gly Glu Asn	
130 135 140	
GAG AAC CTC ATC CCG GGG TCA CCC TTT GAT GTA GTC ACC CAG TCC CCG	478
Glu Asn Leu Ile Pro Gly Ser Pro Phe Asp Val Val Thr Gln Ser Pro	
145 150 155	
GCT CTG CAG AGT TCT CCC GGA TCA CAC AAC CAG AAT TAG	517
Ala Leu Gln Ser Ser Pro Gly Ser His Asn Gln Asn	
160 165 170	

(2) INFORMATION FOR SEQ ID NO:26:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 580 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
 - (A) NAME/KEY: CDS
 - (B) LOCATION: 1..580

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

CAA GTA CTG ATG GCT GCT GCA AGC TTT GGC GAA CGT AAA ATC CCT AAG	48
Gln Val Leu Met Ala Ala Ala Ser Phe Gly Glu Arg Lys Ile Pro Lys	
1 5 10 15	

GGA AAT GGC CCT TAT TCC GTT GGT TGT ACA GAC TTA ATG TTT GAT TAC	96
Gly Asn Gly Pro Tyr Ser Val Gly Cys Thr Asp Leu Met Phe Asp Tyr	
20 25 30	
ACT AAA AAG GGC ACC TTC TTG CGT TTA TAT TAT CCA TCC CAA GAT GAT	144
Thr Lys Lys Gly Thr Phe Leu Arg Leu Tyr Tyr Pro Ser Gln Asp Asp	
35 40 45	
GAT CGC CTT GAC ACC CTT TGG ATC CCA AAT AAG GAG TAT TTT TGG GGT	192
Asp Arg Leu Asp Thr Leu Trp Ile Pro Asn Lys Glu Tyr Phe Trp Gly	
50 55 60	
CTT AGC AAG TAT CTT GGA AAA CAC TGG CTT ATG GGC AAC ATT TTG AGT	240
Leu Ser Lys Tyr Leu Gly Lys His Trp Leu Met Gly Asn Ile Leu Ser	
65 70 75 80	
TTA CTC TTT GGT TCA GTG ACA ACT CCT GCA AAC TGG AAT TCC CCT CTG	288
Leu Leu Phe Gly Ser Val Thr Thr Pro Ala Asn Trp Asn Ser Pro Leu	
85 90 95	
AGG CCT GGT GAA AAA TAC CCA CTT GTT GTT TTT TCT CAT GGT CTT GGA	336
Arg Pro Gly Glu Lys Tyr Pro Leu Val Val Phe Ser His Gly Leu Gly	
100 105 110	
GCA TTC AGG ACA ATT TAT TCT GCT ATT GGC ATT GAC CTG GCA TCT CAT	384
Ala Phe Arg Thr Ile Tyr Ser Ala Ile Gly Ile Asp Leu Ala Ser His	
115 120 125	
GGG TTT ATA GTT GCT GCT GTA GAA CAC AGA GAT AGA TCT GCA TCT GCA	432
Gly Phe Ile Val Ala Ala Val Glu His Arg Asp Arg Ser Ala Ser Ala	
130 135 140	
ACT TAC TAT TTC AAG AAC CAA TCT GCT GCA GAA ATA GGG AAA AAG TCT	480
Thr Tyr Tyr Phe Lys Asn Gln Ser Ala Ala Glu Ile Gly Lys Lys Ser	
145 150 155 160	
TGG CTC TAC CTT AGA ACC CTG AAA GAA GAG GAG GAG ATA CAT ATA CGA	528
Trp Leu Tyr Leu Arg Thr Leu Lys Glu Glu Glu Ile His Ile Arg	
165 170 175	
AAT AAG CAG GTA CGA CAA AGA GCA AAA GAA TGT TCC CAA GCT CTC AGT	576
Asn Lys Gln Val Arg Gln Arg Ala Lys Glu Cys Ser Gln Ala Leu Ser	
180 185 190	
CTG A	580
Leu	

(2) INFORMATION FOR SEQ ID NO:27:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 5 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Gly Xaa Ser Xaa Gly
 1 5

(2) INFORMATION FOR SEQ ID NO:28:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 41 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

TATTCTAGAA TTATGATACA AGTATTAATG GCTGCTGCAA G

41

(2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 32 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

ATTGATATCC TAATTGTATT TCTCTATTCC TG

32

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1335 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

ATGGTACCCC CAAAGCTGCA CGTCCTGTTT TGTCTGTGTG GATGTCTCGC CGTCGTGTAC	60
CCCTTCGATT GGCAGTATAT CAACCCCGTG GCTCACATGA AGACGACCGC CTGGGTGAAT	120
AAGATCCAGG TGCTCATGGC CGCACCAAGC TTCGGTCAGA CCAAGATTCC TAGAGGCAAC	180
GGCCCCTACA GCGTGGGCTG CACCGATCTG ATGTTTCGACC ATACCAACAA AGGAACTTTT	240
CTGAGACTGT ACTACCCCGAG CCAGGACAAC GACAGACTGG ATACTCTGTG GATCCCAAAT	300
AAAGAATATT TTTGGGGTCT TAGCAAATTT CTTGGAACAC ACTGGCTTAT GGGCAACATT	360
TTGAGGTTAC TCTTTGGTTC AATGACAACT CCTGCAAAC GGAATTCCCC TCTGAGGCCT	420
GGTGAAAAAT ATCCAATTGT TGTTTTTTCT CATGGTCTTG GGGCATTTCAG GACACTTTAT	480
TCTGCTATTG GCATTGACCT GGCATCTCAT GGGTTTATAG TTGCTGCTGT AGAACACAGA	540
GATAGATCTG CATCTGCAAC TTAATAATTC AAGGACCAAT CTGCTGCAGA AATAGGGGAC	600
AAGTCTTGGC TCTACCTTAG AACCCGAAA CAAGAGGAGG AGACACATAT ACGAAATGAG	660
CAGGTACGGC AAAGAGCAAA AGAATGTTCC CAAGCTCTCA GTCTGATTCT TGACATTGAT	720
CATGGAAGC CAGTGAAGAA TGCATTAGAT TTAAAGTTTG ATATGGAACA ACTGAAGGAC	780

TCTATTGATA	GGGAAAAAAT	AGCAGTAATT	GGACATTCTT	TTGGTGGAGC	AACGGTTATT	84C
CAGACTCTTA	GTGAAGATCA	GAGATTCAGA	TGTGGTATTG	CCCTGGATGC	ATGGATGTTT	90C
CCACTGGGTG	ATGAAGTATA	TTCCAGAATT	CCTCAGCCCC	TCTTTTTTAT	CAACTCTGAA	960
TATTTCCAAT	ATCCTGCTAA	TATCATAAAA	ATGAAAAAAT	GCTACTCACC	TGATAAAGAA	1020
AGAAAGATGA	TTACAATCAG	GGGTTCAGTC	CACCAGAATT	TTGCTGACTT	CACTTTTGCA	1080
ACTGGCAAAA	TAATTGGACA	CATGCTCAAA	TTAAAGGGAG	ACATAGATTC	AAATGTAGCT	1140
ATTGATCTTA	GCAACAAAGC	TTCATTAGCA	TTCTTACAAA	AGCATTTAGG	ACTTCATAAA	1200
GATTTTGATC	AGTGGGACTG	CTTGATTGAA	GGAGATGATG	AGAATCTTAT	TCCAGGGACC	1260
AACATTAACA	CAACCAATCA	ACACATCATG	TTACAGAACT	CTTCAGGAAT	AGAGAAATAC	1320
AATTAGGATT	CTAGA					1335